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STIC-Biotech/ChemLib

From: Gibbs, Terra
Sent: Friday, November 08, 2002 1:18 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search....

1. Could you please do an oligomer search of Serial number 09/918026 (SEQ ID NO: 3)

2. Please do a length limited search of 100 nucleobases or less.

AND OR ALSO
Terra Gibbs #79523
AU 1635 ✓
Mailbox 11E12 ✓
306-3221

THANK YOU!

*out limit
please*

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 6A04
703-308-3534

Dear Ms. Gibbs

I assumed perhaps incorrectly that you wanted one search run of an oligomer with a size limit of 100 or less.

If you wanted 2 searches

1. an oligomer
2. a length limited search

please let me know & I'll redo this for you. In future if you could number the various pieces of your request as shown above this would be a clearer indicator of the different pieces of your search. This is what most other examiners do to differentiate the various queries.

Thanks.

Toby Port
308-3534

Alternatively, start the next request with the word Also or AND.

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 11/12
Date Completed: 11/15
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

NO PAGE BLANK (USPTO)

GenCore version 5.1.3
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES							
	Result No.	Score	Query Match	Length	DB	ID	Description
OM nucleic - nucleic search, using sw model	1	63	4.0	100	9	F331502S04	AF331505 Homo sapi
Run on: November 14, 2002, 18:57:56 ; Search time 2874 Seconds	2	58	3.7	96	9	F331502S02	AF331503 Homo sapi
(without alignments)	3	55	3.5	100	9	F331502S07	AF331508 Homo sapi
15888.066 Million cell updates/sec	4	54	3.4	90	9	F331502S15	AF331516 Homo sapi
Title: us-09-918-026A-3	5	49	3.1	91	9	F331502S09	AF331510 Homo sapi
Perfect score: 1569	c	6	18	83	9	HSA277254	Homo sapi
Sequence: 1 atggaggccaggccggccccg.....cttggtcctqccatcacctag 1569	c	7	15	1.0	18	E25757	Method for
Scoring table: OLIGO_NUC	c	8	15	1.0	20	AX418779	Sequence
GapOp 60.0 , Gapext 60.0	c	9	15	1.0	24	AX42805	Sequence
Searched: 2054640 seqs, 14551402878 residues	c	10	15	1.0	25	AX223975	Sequence
Word size : 0	c	11	15	1.0	30	E30087	Human BRP-7
Total number of hits satisfying chosen parameters: 995600	c	12	15	1.0	31	AX247925	Sequence
Minimum DB seq length: 0	c	13	15	1.0	31	AX398736	Sequence
Maximum DB seq length: 100	c	14	15	1.0	32	A84491	Sequence 10
Post processing: Listing first 45 summaries	c	15	15	1.0	32	AX427390	Sequence 21
Database : GenEmbl:*	c	16	15	1.0	40	A48829	Sequence .
1: gb_ba:*	c	17	15	1.0	51	AX157211	Sequence .
2: gb_htg:*	c	18	15	1.0	51	AX157212	Sequence .
3: gb_ln:*	c	19	15	1.0	51	AX164830	Sequence
4: gb_oni:*	c	20	15	1.0	51	AX199127	Sequence
5: gb_ov:*	c	21	15	1.0	51	AX199128	Sequence
6: gb_Pat:*	c	22	15	1.0	51	AX392886	Sequence
7: gb_ph:*	c	23	15	1.0	56	AX473971	Sequence
8: gb_pl:*	c	24	15	1.0	66	AX288040	Sequence
9: gb_pr:*	c	25	15	1.0	76	AR030464	Sequence
10: gb_ro:*	c	26	15	1.0	80	AR030463	Sequence
11: gb_sts:*	c	27	15	1.0	87	E27048	Novel recep
12: gb_sy:*	c	28	15	1.0	87	14	APHBSPA
13: gb_un:*	c	29	15	1.0	87	14	APHBTEF
14: gb_i:*	c	30	15	1.0	87	14	APHBPT
15: em_ba:*	c	31	15	1.0	87	14	APHVD23A5
16: em_fun:*	c	32	15	1.0	87	14	APHVBEP
17: em_num:*	c	33	15	1.0	93	6	AX038944
18: em_in:*	c	34	14	0.9	18	6	AR188967
19: em_mu:*	c	35	14	0.9	18	6	I69013
20: em_on:*	c	36	14	0.9	19	6	AX353169
21: em_or:*	c	37	14	0.9	19	6	AX363014
22: em_ov:*	c	38	14	0.9	20	6	AR212087
23: em_Pat:*	c	39	14	0.9	20	6	AX297105
24: em_ph:*	c	40	14	0.9	21	6	AR151133
25: em_pl:*	c	41	14	0.9	21	6	AX027595
26: em_ro:*	c	42	14	0.9	23	6	AR143731
27: em_sts:*	c	43	14	0.9	23	6	BD008422
28: em_un:*	c	44	14	0.9	24	6	AR092060
29: em_yi:*	c	45	14	0.9	24	6	AR112195

ALIGNMENTS

RESULT 1	F331502S04	LOCUS	F331502S04	DNA linear	PRI 13-MAR-2001
		DEFINITION	Hom sapiens acyl-CoA:cholesterol acyltransferase-2 (SOAT2), gene, exon 4.		
ACCESSION	AF331505	VERSION	AF331505_1	GI:13310366	
KEYWORDS		SEGMENT	4 of 15		
		SOURCE	Hom sapiens		
		ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
REFERENCE	1 (bases 1 to 100)	AUTHORS	Katsuren,K., Tamura,T., Arashiro,R., Matsuura,T.,		

Pred. No. is the number of results predicted by chance to have a

Query Match 1.0%; Score 15; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 TGGCCCCACCMCCCC 259
 Db 20 TGCCCCCACCC 6

ORIGIN
 Query Match 1.0%; Score 15; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.8e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 TGGCCCCACCMCCCC 259
 Db 20 TGCCCCCACCC 6

RESULT 9
 AX428505/C
 Locus Sequence 71, from Patent WO0233084.
 Definition AX428505
 Accession AX428505
 Version AX428505.1 GI:21538454

KEYWORDS SOURCE
 ORGANISM synthetic construct.
 artificial sequences.

REFERENCE 1
 AUTHORS Reid, M.E., Gubin, A. and Miller, J.L.
 TITLE Identification of the dombrok blood group glycoprotein as a polymorphic member of the adp-ribosyltransferase gene family
 JOURNAL Patent: WO 0233084-A1 25-APR-2002;
 NEW YORK BLOOD CT (US); GOVERNMENT OF THE UNITED STATES (US)
 FEATURES Location/Qualifiers
 1..24 /organism="synthetic construct"
 source

COMMENT ,
 JOURNAL SRL INC
 REFERENCE 1
 AUTHORS Masakazu M., Kazunasa H., Kenichi O. and Masashi M.
 TITLE Method for the type classification of hepatitis B viruses and
 primer and probe to be used thereon
 JOURNAL Patent: JP 1999103898-A 14-20-APR-1999;
 COMMENT ,
 JOURNAL SRL INC
 REFERENCE 1
 AUTHORS Masakazu M., Kazunasa H., Kenichi O., MASASHI MIZOUE PC
 C12Q1/70, C12N15/09, G01N33/576, C12N15/00
 CC Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 1..18 /organism="Unidentified".
 FT Source
 FEATURES Source
 FT Location/Qualifiers
 1..18 /organism="Unidentified"
 /db_xref="taxon:3264"
 BASE COUNT 5 a 6 c 3 g 4 t
 ORIGIN

Query Match 1.0%; Score 15; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1280 TCCCTGGTCGCCAG 1294
 Db 19 TCCCTGGTCGCCAG 5

RESULT 10
 AX223975/C
 Locus Sequence 16 from Patent WO0157221.
 Definition AX223975
 Accession AX223975.1 GI:15551642
 Version
 KEYWORDS SOURCE synthetic construct.
 ORGANISM synthetic construct.
 artificial sequences.

REFERENCE 1
 AUTHORS Luche, R.M. and Wel,B.
 TITLE Dsp-12 and dsp-13 dual-specificity phosphatases
 JOURNAL Patent: WO 0157221-A 16 09 AUG-2001;
 Cepyr, Inc. (US)
 FEATURES Location/Qualifiers
 1..25 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="P-Primer"
 BASE COUNT 4 a 3 c 15 g 3 t
 ORIGIN

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 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 244 CTGCCCCACCTCCC 258
 Db 22 CTGCCCCACCTCCC 8

RESULT 8
 AX418779/C
 Locus Sequence 174 from Patent WO0210378.
 Definition AX418779
 Accession AX418779.1 GI:21523642
 Version
 KEYWORDS SOURCE synthetic construct.
 ORGANISM synthetic construct.
 artificial sequences.

REFERENCE 1
 AUTHORS Cowser, L.M., Wyatt, J., Freier, S.M., Monia, B.P., Butler, M.M. and McKay, R.
 Title Antisense modulation of Ptp1b expression
 JOURNAL Patent: WO 010378-A 174 07-FEB-2002;
 ISIS PHARMACEUTICALS, INC. (US)
 FEATURES Location/Qualifiers
 1..20 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Antisense Oligonucleotide"
 BASE COUNT 2 a 3 c 13 g 2 t

RESULT 11
 E30087 LCUS Human BMP-7 promoter and method for detecting bone-associated substance by using the same. PAT 18-JUN-2001
 DEFINITION substance by using the same Human BMP-7 promoter and method for detecting bone-associated substance by using the same.
 ACCESSION E30087
 VERSION E30087.1
 KEYWORDS unclassified
 SOURCE
 ORGANISM unclassified
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Shiraii, K. and Takeyuki, S.
 TITLE Human BMP-7 promoter and method for detecting bone-associated substance by using the same
 JOURNAL Patent: JP 1999313675-A 2 16-NOV-1999;
 COMMENT HOECHST MARION ROUSSEL GMBH
 OS Unidentified
 PN JP 1999313675-A/2
 PD 16-NOV-1999
 PF 30-APR-1998 JP 1998120174
 PR SHINJI KAWAI; TAKEYUKI SUGIURA
 PI C12N5/09,C12N5/10,C12Q1/68//A61K48/00, (C12N5/10,C12R1:91), PC
 PC C12N5/00, (C12N5/00,C12R1:91)
 CC Strandedness: Single;
 CC Topology: Linear;
 Key Location/Qualifiers
 FH 1 . .30
 FT source /organism="Unidentified".
 FEATURES source Location/Qualifiers
 1 . .30
 /organism="Unidentified"
 /db_xref="taxon:32044"
 BASE COUNT 4 a 9 c 14 g 3 t
 ORIGIN

Query Match 1.0%; Score 15; DB 6; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 506 CCTGGGTGCCCATGT 520
 Db 31 CCTGGGTGCCCATGT 17

RESULT 13
 AX398736 LOCUS AX398736 Sequence 28 from Patent WO0220786.
 DEFINITION AX398736 Version 31 bp DNA linear
 ACCESSION AX398736_1 GI:21261287
 KEYWORDS SOURCE synthetic construct.
 ORGANISM synthetic construct.
 artificial sequences.

REFERENCE 1
 AUTHORS Schiavo, G.M. and Iglesias, T.I.
 TITLE Kinase d interacting protein
 JOURNAL Patent: WO 0220786 A 28 14-MAR-2002;
 IMPERIAL CANCER RESEARCH TECHNOLOGY LIMITED (GB)

FEATURES Location/Qualifiers
 1 . .31
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Primer"

BASE COUNT 6 a 9 c 4 g 12 t
 ORIGIN

Query Match 1.0%; Score 15; DB 6; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 732 CTCCCTCCCTGAGAGA 746
 Db 17 CTCCCTCCCTGAGAGA 31

RESULT 14
 A84491_1/C LOCUS A84491 Sequence 106 from Patent WO9845704.
 DEFINITION A84491 Version 32 bp DNA linear
 ACCESSION A84491_1 GI:6733410
 KEYWORDS SOURCE unidentified.
 ORGANISM unidentified.
 unclassified.

REFERENCE 1 (bases 1 to 32)
 AUTHORS Tullin, S. and Kasper, A.
 TITLE A METHOD FOR EXTRACTING QUANTITATIVE INFORMATION RELATING TO AN
 INFLUENCE ON A CELLULAR RESPONSE
 JOURNAL Patent: WO 9845704 A 106 15-OCT-1998;
 TULLIN SOBREN (DK); KASPER ALMHOLT (DK)

FEATURES Location/Qualifiers
 1 . .32
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 6 a 12 c 9 g 5 t
 ORIGIN

Query Match 1.0%; Score 15; DB 6; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 749 CTGTGCCTGGATCC 763
 Db 17 CTGTGCCTGGATCC 3

RESULT 12
 AX247925/C LOCUS AX247925 Sequence 4 from Patent WO0166800.
 DEFINITION AX247925 Version 31 bp DNA linear
 ACCESSION AX247925
 VERSION GI:15862548
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 31)
 AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.
 TITLE Human single nucleotide polymorphisms
 Patent: WO 0166800 A 4 13-SEP-2001;
 JOURNAL WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
 FEATURES Location/Qualifiers
 1 . .31
 /organism="Homo sapiens"
 BASE COUNT 8 a 9 c 7 g 6 t 1 others
 ORIGIN

RESULT 15
AX427390/c
LOCUS AX427390
DEFINITION Sequence 106 from Patent EP1199564.
ACCESSION AX427390
VERSION AX427390.1 GI:21530743
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1.
AUTHORS Thastrup,O., Bjoern,S.P., Tullin,S., Almbolt,K. and Scudder,K.
TITLE A method for screening substances for effect on intracellular
translocation
JOURNAL Patent: EP1199564-A 106 24-APR-2002;
FEATURES BioImage A/S (DK)
source Location/Qualifiers
1..32
organism="unidentified"
/db_xref="taxon:3264"
BASE COUNT 6 a 12 c 9 g 5 t
ORIGIN
Query Match 1.0%; Score 15; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 749 CTGTGCTGGATCC 763
||| ||| ||| ||| |||
Db 17 CTGTGCTGGATCC 3

Search completed: November 14, 2002, 20:23:03
Job time : 2877 secs

Result No.	Score	Query	Match	Length	DB ID	Description	SUMMARIES
1	60	3.8	60	24	ABN36849	Human spliced tran	PD 07-FEB-2002.
2	24	1.5	25	21	AAAT6178	Human ACAT Related	XX XX
3	23	1.5	23	21	AAAT6183	Human ACAT Related	PR 20-JUL-2001; 2001WO-IB01903.
4	20	1.3	20	21	AAAT5763	Human acyl CoA:cho	PA (COMP-) COMPUGEN INC.
c	20	1.3	20	21	AAAT57364	Human acyl CoA:cho	XX PR 28-JUL-2000; 2000US-221607P.
6	17	1.1	65	24	ABN28762	Rat spliced transci	XX DR 02-MAY-2001; 2001US-287724P.
7	16	1.0	20	21	AAZ71373	Human biallelic ma	XX PT New oligonucleotide libraries comprising oligonucleotides which
8	16	1.0	60	19	AAV21372	Immunoglobin genom	PT selectively hybridize to mRNAs transcribed from a transcription unit of
9	16	1.0	87	22	ABA50541	Human breast cell	PT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Listing first 45 summaries
Database : N_Geneseq-101002:
1: /SIDS2/gcdata/geneseq/geneseq -emb1/NA1980.DAT :*
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4: /SIDS2/gcdata/geneseq/geneseq -emb1/NA1983.DAT :*
5: /SIDS2/gcdata/geneseq/geneseq -emb1/NA1984.DAT :*
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23: /SIDS2/gcdata/geneseq/geneseq -emb1/NA2001B.DAT :*
24: /SIDS2/gcdata/geneseq/geneseq -emb1/NA2002.DAT :*

RESULT 1
ID ABN36849 standard; DNA; 60 BP.
XX ABN36849;
XX DT 15-JUL-2002 (first entry)
DE Human spliced transcript detection oligonucleotide SEQ ID NO:9597.
XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:9597.
XX KW Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.
XX OS Homo sapiens.
XX PN WO200210449-A2.

XX PD 07-FEB-2002.

XX PF 20-JUL-2001; 2001WO-IB01903.

XX PR 28-JUL-2000; 2000US-221607P.

XX PR 02-MAY-2001; 2001US-287724P.

XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX DR WPI: 2002-257383/30.

PT a genome, useful for detecting tissue-, pathology-, and
 PT developmental-specific genes -
 XX Example 1; SEQ ID 9597; 47pp; English.
 XX The present invention describes oligonucleotide libraries for detecting
 CC messenger RNAs that populate the (sub-)transcriptome, where the transcriptome
 CC comprises messenger RNAs transcribed from multiple
 CC transcription units that comprise a genome. The library comprises
 CC several oligonucleotides, each capable of hybridising selectively to a
 CC set of messenger RNAs transcribed from a given transcription unit of
 CC the genome, which encodes one or more messenger RNA splice variants.
 CC The oligonucleotide libraries are useful for detecting mRNAs from a
 CC biological sample, in expression profiling studies, in qualitatively or
 CC quantitatively characterising the corresponding transcriptome, and in
 CC detecting RNA transcripts and splice variants of human or animal
 CC transcriptomes. The libraries may also be used as specialised mini
 CC libraries to detect transcripts of a sub-transcriptome under a
 CC particular biological or pathological state, and so allowing the
 CC detection of tissue- and pathology-specific genes such as those genes
 CC only expressed in specific tissue under a specific pathological
 CC condition; to detect developmental specific genes; and to detect RNA
 CC transcripts and splice variants of a transcriptome of a patient suffering
 CC from a particular disorder. ABN27253 to ABN59589 represent
 CC oligonucleotide sequences from rats, humans and mice, which are used in
 CC the exemplification of the present invention.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 60 BP; 7 A; 21 C; 10 G; 22 T; 0 other;

Query Match 3.8%; Score 60; DB 24; Length 60;
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1017 TATCCCTGCATGCAAGTGGCATCUTCAGCTGCTCATCTTCCTTCCT 1076
 Db 1 TATCCCTGCATGCAAGTGGCATCUTCAGCTGCTCATCTTCCTTCCT 60
 XX

RESULT 2
 AAA76178 standard; DNA; 25 BP.
 XX AC AAA76178;
 XX DT 14-DEC-2000 (first entry)
 XX DE Human ACAT Related Gene Product 2 ARG P2 PCR primer 206.
 XX KW Human; ACAT Related Gene Product 2; ARG P2;
 KW enzyme; acyl Coenzyme A-cholesterol acyltransferase 1; ACAT1;
 KW sterol esterification; lipid homeostasis; diacylglycerol acyltransferase;
 KW DGAT; PCR primer; ss.
 OS Homo sapiens.
 PN US6100077-A.
 XX PD 08-AUG-2000.
 XX PF 01-OCT-1998; 98US-0165042.
 XX PR 01-OCT-1998; 98US-0165042.
 XX PA (UYCO) UNIV COLUMBIA NEW YORK.
 PI Sturley SL, Oelkers P;
 XX DR 2000-557622/51.
 PT New nucleic acid encoding a human diacylglycerol acyltransferase, or
 PT other diseases associated with an imbalance of triglyceride levels -
 XX Disclosure; Column 17; 32pp; English.
 PS

XX The enzyme acyl Coenzyme A-cholesterol acyltransferase 1 (ACAT1)
 CC mediates sterol esterification, an important component of intracellular
 CC lipid homeostasis. The present invention relates to human ACAT Related
 CC Gene Product 2 (ARGP2). ARG P2 is a diacylglycerol acyltransferase
 CC (DGAT). ARG P2 is a tissue specific sterol esterification enzyme. The
 CC present sequence is a PCR primer used to isolate ARG P2 coding sequence
 CC (see AAA76170).
 XX Sequence 23 BP; 3 A; 9 C; 5 G; 6 T; 0 other;
 DR Query Match 1.5%; Score 23; DB 21; Length 23;
 XX Best Local Similarity 100.0%; Pred. No. 1;
 PT New nucleic acid encoding a human diacylglycerol acyltransferase,
 XX DR 2000-557622/51.
 XX PA (UYCO) UNIV COLUMBIA NEW YORK.
 PI Sturley SL, Oelkers P;
 XX DR WPI: 2000-557622/51.
 XX PA New nucleic acid encoding a human diacylglycerol acyltransferase,

XX
PD 26-FEB-1998.
XX
PF 15-AUG-1997; 97WO-US15485.
XX
PR 19-AUG-1996;
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Fujieda S, Ke Z, Saxon AW;
XX
DR WPI: 1998-179050/16.
XX
New immunoglobulin trans-spliced transcripts - used for, e.g. stimulating or inhibiting synthesis of particular immunoglobulin isotype, useful for treating immune disorders
XX
Example 2; Page 36; 83PP; English.
XX
The nucleotides AV21362-V21373 are examples of the genomic fragments from which sequences were used to create trans-spliced transcripts. The transcripts comprise a sequence capable of annealing to a human genomic immunoglobulin (Ig) heavy chain I region of a locus selected from mu, epsilon, alpha and gamma followed by a second sequence capable of annealing to a region of a second locus selected from mu, epsilon, alpha and gamma as above. The products can be used for stimulating or inhibiting synthesis of a particular human Ig isotype. They can be used for treating disorders mediated by IgM, IgG, IgA or IgE, in particular for inhibiting IgE synthesis or isotype switching to IgE for treating allergic disorders. They can also be used for treating autoimmune and alloimmune diseases amongst others.
XX
Sequence 60 BP; 16 A; 8 C; 30 G; 6 T; 0 other;
XX
Query Match 1.0%; Score 16; DB 19; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 30 GCAGAGGACAGAAGGG 45
Db 40 GCAGAGGACAGAAGGG 55
XX
RESULT 9
ID ABA50541 standard; DNA; 87 BP.
AC ABA50541;
XX
DT 01-JAN-2001 (first entry)
XX
DE Human breast cell single exon nucleic acid probe #9236.
XX
KW Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00662.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-007456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632166.
PR 21-SEP-2000; 2000US-0334687.
PR 27-SEP-2000; 2000US-0236559.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
PS Claim 4; SEQ ID NO 9236; 327PP + sequence listing; English.
XX
The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosticating breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 87 BP; 25 A; 17 C; 28 G; 17 T; 0 other;
XX
Query Match 1.0%; Score 16; DB 22; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 134 TGGAGGCTGTGAAGGC 149
Db 5 TGGAGGCTGTGAAGGC 20
XX
RESULT 10
ABA68500 standard; DNA; 87 BP.
ID ABA68500
XX
AC ABA68500;
XX
DT 01-FEB-2002 (first entry)
XX
DE Human foetal liver single exon nucleic acid probe #16805.
XX
KW Human; foetal liver; gene expression; breast;
KW Homo sapiens.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-020456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632166.
PR 21-SEP-2000; 2000US-0236539.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX

WPI: 2001-483447/52.
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human fetal liver -
 XX SEQ ID NO 16805; 639pp + sequence listing; English.
Claim 4: SEQ ID NO 16805; 639pp + sequence listing; English.
 The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC fetal liver. The present sequence is a single exon nucleic acid
 CC probe of the invention.
 Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 87 BP; 25 A; 17 C; 28 G; 17 T; 0 other;
 SQ Query Match 1.0%; Score 16; DB 22; Length 87;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 134 TGAGGCTGTGAAGC 149
 Db 5 TGAGGCTGTGAAGC 20
 XX RESULT 11
 ABA35481 standard; DNA; 87 BP.
 ID ABA35481
 XX AC ABA35481;
 XX DT 23-JAN-2002 (first entry)
 XX DE Probe #13947 for gene expression analysis in human heart cell sample.
 KW Human; gene expression; heart; microarray; vascular system; probe;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease; ss.
 XX OS Homo sapiens.
 PN WO200157274-A2.
 XX PD 09-AUG-2001.
 XX PF 30-JAN-2001; 2001WO-US00666.
 XX PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0180312.
 PR 30-JUN-2000; 2000US-0207456.
 PR 03-AUG-2000; 2000US-0608408.
 PR 21-SEP-2000; 2000US-0632366.
 PR 27-SEP-2000; 2000US-0234687.
 PR 04-OCT-2000; 2000US-0235359.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-488899/53.
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts -
 PT Claim 4; SEQ ID NO 13947; 530pp; English.
 XX The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart. The
 CC present sequence is one such probe. The probes may be used for
 predicting, measuring and displaying gene expression in samples derived
 XX SQ Sequence 87 BP; 25 A; 17 C; 28 G; 17 T; 0 other;
 CC Query Match 1.0%; Score 16; DB 22; Length 87;
 CC Best Local Similarity 100.0%; Pred. No. 2.3e+03;

CC from the human heart via microarrays. By measuring gene expression, the
 CC probes are useful for predicting, diagnosing, grading, staging,
 CC monitoring and prognosing diseases of the human heart and vascular system
 e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
 CC congenital heart disease.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 87 BP; 25 A; 17 C; 28 G; 17 T; 0 other;
 SQ Query Match 1.0%; Score 16; DB 22; Length 87;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 134 TGAGGCTGTGAAGC 149
 Db 5 TGAGGCTGTGAAGC 20
 XX RESULT 12
 AAK16867
 ID AAK16867 standard; DNA; 87 BP.
 XX AC AAK16867;
 XX DT 05-NOV-2001 (first entry)
 XX DE Human brain expressed single exon probe SEQ ID NO: 16858.
 XX KW Human; brain expressed exon; gene expression analysis; probe;
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 KW epilepsy; cancer; ss.
 XX OS Homo sapiens.
 XX PN WO200157275-A2.
 XX PD 09-AUG-2001.
 XX XX 30-JAN-2001; 2001WO-US00667.
 XX PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0638408.
 PR 03-AUG-2000; 2000US-0532366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0235359.
 PR 04-OCT-2000; 2000US-0024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-483446/52.
 XX PT Single exon nucleic acid probes for analyzing gene expression in human
 PT brains -
 XX PS Example 4; SEQ ID NO: 16858; 650pp + Sequence Listing; English.
 XX CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is one of the probes of the
 CC invention.
 XX SQ Sequence 87 BP; 25 A; 17 C; 28 G; 17 T; 0 other;
 CC Query Match 1.0%; Score 16; DB 22; Length 87;
 CC Best Local Similarity 100.0%; Pred. No. 2.3e+03;

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OM nucleic - nucleic search, using sw model

Run on: November 14, 2002, 19:31:36 ; Search time 63 Seconds

(without alignments)
9202.612 Million cell updates/sec

Title: US-09-918-026a-3

Perfect score: 1569

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Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 328367 seqs, 184756068 residues

Word size : 0

Total number of hits satisfying chosen parameters : 189978

Minimum DB seq length: 0

Maximum DB seq length: 100

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4: /cgn2_6/podata/1/pubnpa/us06_pubcomb.seq;*
5: /cgn2_6/podata/1/pubnpa/pct5_new_pub.seq;*
6: /cgn2_6/podata/1/pubnpa/us07_pubcomb.seq;*
7: /cgn2_6/podata/1/pubnpa/us08_new_pub.seq;*
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9: /cgn2_6/podata/1/pubnpa/us09_new_pub.seq;*
10: /cgn2_6/podata/1/pubnpa/us09_pubcomb.seq;*
11: /cgn2_6/podata/1/pubnpa/us10_new_pub.seq;*
12: /cgn2_6/podata/1/pubnpa/us10_pubcomb.seq;*
13: /cgn2_6/podata/1/pubnpa/us10_new_pub.seq;*
14: /cgn2_6/podata/1/pubnpa/us10_pubcomb.seq;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	16	1.0	87	10	US-09-761-20801		Sequence 2301, A
c 2	15	1.0	20	10	US-09-883-174		Sequence 174, App
c 3	15	1.0	25	10	US-09-775-925-16		Sequence 16, App
c 4	15	1.0	31	10	US-09-774-4		Sequence 4, App
c 5	15	1.0	51	10	US-09-888-123-20		Sequence 20, App
c 6	14	0.9	24	10	US-09-919-060-25		Sequence 25, App
c 7	14	0.9	25	10	US-09-292-973-8		Sequence 8, App
c 8	14	0.9	30	10	US-09-888-541-18		Sequence 18, App
c 9	14	0.9	36	10	US-09-815-837-104		Sequence 101, App
c 10	14	0.9	47	10	US-09-785-632A-6		Sequence 6, App
c 11	14	0.9	47	10	US-09-888-123-24		Sequence 24, App
c 12	14	0.9	68	10	US-09-878-574-3227		Sequence 3227, App
c 13	14	0.9	82	10	US-09-864-761-2451B		Sequence 2451B, A
c 14	14	0.9	88	10	US-09-920-300A-1141		Sequence 1141, Ap
c 15	14	0.9	88	12	US-10-033-528-1141		Sequence 1141, Ap
c 16	14	0.9	90	10	US-09-853-666-26		Sequence 666, App
c 17	14	0.9	98	10	US-09-864-761-3349		Sequence 2349, A
c 18	14	0.9	98	10	US-09-815-242-3561		Sequence 3561, Ap
c 19	14	0.9	98	10	US-09-878-574-12594		Sequence 12594, A

SEQUENCES

c 20	14	0.9	99	10	US-09-815-242-3511	Sequence 3511, Ap
c 21	13	0.8	17	10	US-09-866-108-2293	Sequence 2293, Ap
c 22	13	0.8	17	10	US-09-866-108-2294	Sequence 2294, Ap
c 23	13	0.8	17	10	US-09-866-108-2295	Sequence 2295, Ap
c 24	13	0.8	17	10	US-09-866-108-2296	Sequence 2296, Ap
c 25	13	0.8	17	10	US-09-866-108-2297	Sequence 2297, Ap
c 26	13	0.8	18	10	US-09-977-432-9	Sequence 9, Appl
c 27	13	0.8	18	10	US-09-961-53-9	Sequence 9, Appl
c 28	13	0.8	18	10	US-09-967-624-16	Sequence 16, Appl
c 29	13	0.8	18	12	US-10-014-220-9	Sequence 9, Appl
c 30	13	0.8	20	10	US-09-215-652-25	Sequence 25, Appl
c 31	13	0.8	20	10	US-09-817-913-22	Sequence 22, Appl
c 32	13	0.8	20	10	US-09-350-559-50	Sequence 50, Appl
c 33	13	0.8	20	10	US-09-866-108-5222	Sequence 222, Ap
c 34	13	0.8	21	10	US-09-823-825A-2	Sequence 2, Appl
c 35	13	0.8	24	10	US-09-969-73-259	Sequence 3259, Ap
c 36	13	0.8	24	10	US-09-885-441-43	Sequence 43, Appl
c 37	13	0.8	24	10	US-09-901-106-24	Sequence 24, Appl
c 38	13	0.8	25	10	US-09-866-108-5223	Sequence 5223, Ap
c 39	13	0.8	25	10	US-09-866-108-5224	Sequence 5224, Ap
c 40	13	0.8	25	10	US-09-866-108-5225	Sequence 5225, Ap
c 41	13	0.8	25	10	US-09-866-108-5226	Sequence 5226, Ap
c 42	13	0.8	25	10	US-09-866-108-5227	Sequence 5227, Ap
c 43	13	0.8	25	10	US-09-866-108-5228	Sequence 5228, Ap
c 44	13	0.8	25	10	US-09-866-108-5229	Sequence 5229, Ap

ALIGNMENTS

RESULT 1	US-09-864-761-20801	Sequence 20801, Application US/09864761
		; GENERAL INFORMATION:
		; APPLICANT: Penn, Sharron G.
		; APPLICANT: Rank, David R.
		; APPLICANT: Hanelz, David K.
		; APPLICANT: Chen, Weisheng
		; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR EXPRESSION ANALYSIS BY MICROARRAY
		; FILE REFERENCE: Aeomica-X-1
		; CURRENT APPLICATION NUMBER: US/09/864,761
		; CURRENT FILING DATE: 2001-05-23
		; PRIORITY APPLICATION NUMBER: US 60/180,312
		; PRIORITY FILING DATE: 2000-02-04
		; PRIORITY APPLICATION NUMBER: US 60/207,456
		; PRIORITY FILING DATE: 2000-05-26
		; PRIORITY APPLICATION NUMBER: US 09/632,366
		; PRIORITY FILING DATE: 2000-08-03
		; PRIORITY APPLICATION NUMBER: GB 24263, 6
		; PRIORITY FILING DATE: 2000-10-04
		; PRIORITY APPLICATION NUMBER: US 60/236,359
		; PRIORITY FILING DATE: 2000-09-27
		; PRIORITY APPLICATION NUMBER: PCT/US01/00666
		; PRIORITY FILING DATE: 2001-01-30
		; PRIORITY APPLICATION NUMBER: PCT/US01/00667
		; PRIORITY FILING DATE: 2001-01-30
		; PRIORITY APPLICATION NUMBER: PCT/US01/00668
		; PRIORITY FILING DATE: 2001-01-30
		; PRIORITY APPLICATION NUMBER: PCT/US01/00669
		; PRIORITY FILING DATE: 2001-01-30
		; PRIORITY APPLICATION NUMBER: PCT/US01/00665
		; PRIORITY FILING DATE: 2001-01-30
		; PRIORITY APPLICATION NUMBER: PCT/US01/00662
		; PRIORITY FILING DATE: 2001-01-30
		; PRIORITY APPLICATION NUMBER: PCT/US01/00663
		; PRIORITY FILING DATE: 2001-01-30

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; PRIORITY APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: AnnoMax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 20801
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE:
; OTHER INFORMATION: MAP TO AL022308.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.5
; OTHER INFORMATION: EXPRESSED IN HEML100, SIGNAL = 8.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 8.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.7
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; OTHER INFORMATION: SWISSPROT HIT: P80152; EVALUATE 7.10e+00
; OTHER INFORMATION: EST_HUMAN HIT: R09942.1; EVALUATE 1.00e-17
; OTHER INFORMATION: EST_HUMAN HIT: R09942.1; EVALUATE 1.00e-17
; OTHER INFORMATION: NT HIT: U91328.1; EVALUATE 1.00e-11
; OTHER INFORMATION: SWISSPROT HIT: P80152; EVALUATE 7.10e+00
; OTHER INFORMATION: EST_HUMAN HIT: R09942.1; EVALUATE 1.00e-17
; OTHER INFORMATION: EST_HUMAN HIT: R09942.1; EVALUATE 1.00e-17
; SEQ ID NO: 20801
; LENGTH: 87
; TYPE: DNA
; ORGANISM: Homo sapiens

Query Match 1.0%; Score 16; DB 10; Length 87;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 TGAGGCTGTGAAGC 149
Db 5 TGAGGCTGTGAAGC 20

RESULT 2
US-09-854-883-174/C
; Sequence 174, Application US/09854883
; Patent No. US2002005479A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Covert
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/09/854,883
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO: 174
; LENGTH: 20
; TYPE: DNA
; FEATURE: Artificial Sequence
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-854-883-174

Query Match 1.0%; Score 15; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 TGCCCCCACCTCCCC 259
Db 15 TGCCCCCACCTCCCC 259

RESULT 3
US-09-775-925-16/C
; Sequence 16, Application US/09775925
; Patent No. US20010049358A1
; GENERAL INFORMATION:
; APPLICANT: Luche, Ralf M.
; TITLE OF INVENTION: PHOSPHATASES
; FILE REFERENCE: 200125_420
; CURRENT APPLICATION NUMBER: US/09/775,925
; CURRENT FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-775-925-16

Query Match 1.0%; Score 15; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 CTGGCCCCACCCCTCCC 258
Db 22 CTGGCCCCACCCCTCCC 8

RESULT 4
US-09-801-274-4/C
; Sequence 4, Application US/09801274
; Patent No. US2002002319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michelle S.
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825_2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-801-274-4

Query Match 1.0%; Score 15; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 506 CCTGGGTGCCATGT 520
Db 31 CCTGGGTGCCATGT 17

RESULT 5
US-09-898-323-20
; Sequence 20, Application US/09898323
; Patent No. US20020150904A1
; GENERAL INFORMATION:

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APPLICANT: Bi, Wanli
 APPLICANT: Livak, Kenneth J.
 APPLICANT: Bloch, Will
 TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE ASSAY
 FILE REFERENCE: 4599US
 CURRENT APPLICATION NUMBER: US/09/898,323
 CURRENT FILING DATE: 2002-01-16
 PRIOR APPLICATION NUMBER: US 60/216,514
 PRIOR FILING DATE: 2000-07-03
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 20
 LENGTH: 51
 TYPE: DNA
 ORGANISM: Unknown
 OTHER INFORMATION: Complement of SEQ ID NO:2
 US-09-898-323-20

Query Match 1.0%; Score 15; DB 10; Length 51;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 US-09-919-060-25/c
 Sequence 25, Application US/09919060
 GENERAL INFORMATION:
 APPLICANT: Wisnewski, Nancy
 APPLICANT: Brandt, Kevin S.
 TITLE OF INVENTION: CANINE COX-1 AND COX-2 NUCLEIC ACID MOLECULES, PROTEINS AND USES
 FILE REFERENCE: AD-1
 CURRENT APPLICATION NUMBER: US/09/919,060
 CURRENT FILING DATE: 2001-07-31
 PRIOR APPLICATION NUMBER: 60/224,486
 PRIOR FILING DATE: 2000-08-11
 NUMBER OF SEQ ID NOS: 25
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 25
 LENGTH: 24
 TYPE: DNA
 ORGANISM: Artificial sequence
 FEATURE: Synthetic Primer
 OTHER INFORMATION: Synthetic Primer
 US-09-919-060-25

Query Match 0.9%; Score 14; DB 10; Length 24;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 US-09-292-973-8
 Sequence 8, Application US/09292973
 GENERAL INFORMATION:
 APPLICANT: ZASTANYI, Roman L.
 APPLICANT: MCWHINNIE, Elizabeth A.
 TITLE OF INVENTION: No. US20020111473A1el G Protein Coupled Receptor
 FILE REFERENCE: 8074-9004
 CURRENT APPLICATION NUMBER: US/09/292,973
 CURRENT FILING DATE: 1999-04-16
 PRIOR APPLICATION NUMBER: US 60/081,995
 PRIOR FILING DATE: 1998-04-16

Query Match 0.9%; Score 14; DB 10; Length 30;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9
US-09-815-837-104
Sequence 104, Application US/09815837
Patent No. US2002008241A1
GENERAL INFORMATION:
APPLICANT: Carter, Darrick
APPLICANT: Zhu, Shirley
APPLICANT: Arimilli, Subhashini
APPLICANT: Wang, Ajun
Corixa Corporation
TITLE OF INVENTION: Immune Mediators and Related Methods
FILE REFERENCE: 014.058-00567.0US
CURRENT APPLICATION NUMBER: US/09/815.837
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 60/191,274
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: US 60/204,249
PRIOR FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: US 60/264,003
PRIOR FILING DATE: 2001-01-23
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 104
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: phosphorylated
OTHER INFORMATION: Primer 1
NAME/KEY: modified_base
LOCATION: (1)
OTHER INFORMATION: n = 5' phosphorylated C
US-09-815-837-104

Query Match 0.9%; Score 14; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;
Db 15 AGCGGCCACGCCG 2

RESULT 11
US-09-898-323-24
Sequence 24, Application US/09898323
Patient No. US20020150304A1
GENERAL INFORMATION:
APPLICANT: Bi, Wanli
APPLICANT: Livak, Kenneth J.
APPLICANT: Bloch, Will
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE ASSAY
FILE REFERENCE: 45590US
CURRENT APPLICATION NUMBER: US/09/898.323
CURRENT FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: US 60/216,514
PRIOR FILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 24
LENGTH: 47
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Ligation product of probes Ap3 and Ap4 from Scheme IIb, follow
OTHER INFORMATION: cleavage of Ap4
US-09-898-323-24

Query Match 0.9%; Score 14; DB 10; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;
Db 15 AGCGGCCACGCCG 2

RESULT 12
US-09-878-574-3227
Sequence 3227, Application US/09878574
PATENT NO. US20020110548A1
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
PATENT NO. US20020061512A1
FILE REFERENCE: 38-2-(154)1B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO: 3227
LENGTH: 68
TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-014-Q1-B1-C8
US-09-878-574-3227

Query Match 0.9%; Score 14; DB 10; Length 68;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;
Db 15 AGCGGCCACGCCG 2

RESULT 13
US-09-785-632A-6/C
Sequence 6, Application US/09785632A
GENERAL INFORMATION:
APPLICANT: Kim, Jin-Soo
APPLICANT: Kwon, Young Do
APPLICANT: Kim, Hyun-Non
APPLICANT: Ryu, Eun-Hyun
TITLE OF INVENTION: ZINC FINGER DOMAINS AND METHODS OF
TITLE OF INVENTION: IDENTIFYING SAME
FILE REFERENCE: 12279-002001
CURRENT APPLICATION NUMBER: US/09/785,632A
CURRENT FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 166
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 6
LENGTH: 47
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: optimal binding site
US-09-785-632A-6

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Db 27 ATGCTGGTGTGT 40
Best Local Similarity 100 %; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 74 GTGGAGATGAAAC 87
Db 32 GTGGAGATGAAAC 45

RESULT 14
US-09-864-761-24518
; Sequence 1141, Application US/09864761
; Patent No. US20020048763A1
GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Weisheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Lassing Engine vers. 1.1
SEQ ID NO: 24518
LENGTH: 82
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL162260.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
OTHER INFORMATION: EST_ROMAN HIT: AW581997.1, EVALUE 2.50e-01

Best Local Similarity 100 %; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 74 GTGGAGATGAAAC 87
Db 32 GTGGAGATGAAAC 45

RESULT 14
US-09-920-300A-1141/c
; Sequence 1141, Application US/09920300A
; Patent No. US20020136728A1
GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meager, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 1141
; LENGTH: 88
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-920-300A-1141

Query Match 0.9%; Score 14; DB 10; Length 88;
Best Local Similarity 100 %; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 384 CGCTGGCCCTGTGTG 397
Db 29 CGCTGGCCCTGTGTG 16

RESULT 15
US-10-033-528-1141/c
; Sequence 1141, Application US/10033528
; Patent No. US20020131971A1
GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meager, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 1141
; LENGTH: 88
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-1141

Query Match 0.9%; Score 14; DB 12; Length 88;
Best Local Similarity 100 %; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 384 CGCTGGCCCTGTGTG 397
Db 29 CGCTGGCCCTGTGTG 16

Search completed: November 14, 2002, 20:57:26
Job time : 73 secs

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Result No.	Score	Query Match	Length	DB ID	Description
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c 2	17	1.1	80	14 F31995	B1472373 fs02601.Y AA791480 vs66.f11.r
c 3	17	1.1	89	13 B1472373	F24292 HSPD10465 H BH850932 SALK_0721
4	17	1.1	91	9 AA791480	
c 5	17	1.1	93	14 F24292	
c 6	16	1.0	74	17 BH850932	

%

RESULTS

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2002, 19:27:46 ; Search time 1868 Seconds
(without alignments)

13603.168 Million cell updates/sec

Title: US-09-918-026A-3

Perfect score: 1569

Sequence: 1 atggaggccggggccg cttggctctgcattacccat 1569

Scoring table: OLIGO_NUC

Gapext 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 357874

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_estthum:*

3: em_estin:*

4: em_estmu:*

5: em_lestov:*

6: em_lestp1:*

7: em_estro:*

8: em_hnc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_lss:*

18: em_gss_num:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_nam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rcd:*

RESULT 1

AZ920873 LOCUS 71 bp DNA linear GSS 17-DEC-2001 DEFINITION Zea mays sequence.

ACCESSION AZ920873 ORGANISM Zea mays.

VERSION AZ920873.1 KEYWORDS Zea mays.

SOURCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

REFERENCE Walbot, V.

AUTHORS

TITLE Maize genomic sequences found using engineered RescueMu transposon

JOURNAL Unpublished (2001)

COMMENT Contact: Walbot, V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
tel: 650 723 2227
fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation end of ends cut by a single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1006021 row: 38
Class: transposon-tagged.
Location/Qualifiers

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Db	62	CATGGAGGCTGTGAAGG	78
RESULT	4		
LOCUS	AA791480		
DEFINITION	AA791480		
ACCESSION	AA791480		
VERSION	AA791480.1		
KEYWORDS	EST.		
ORGANISM	Mus musculus		
SOURCE	house mouse.		
MATERIAL	AA791480	91 bp	mRNA linear EST 09-FEB-1998
DEFINITION	vs6ff1.r1 stratagene mouse skin (#937313)		Mus musculus cDNA clone
IMAGE:11512775', mRNA sequence.			
JOURNAL			
MEDLINE			
COMMENT			
REFERENCE	1 (bases 1 to 93)		
AUTHORS	Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A., Pandolfi,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.		
TITLE	Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization		
JOURNAL	Genome Res.	6 (1), 35-42 (1996)	
COMMENT	Contact: Valle G.		
CRIBI Biotechnology Centre			
University of Padua			
Via Trieste 75, 35121 Padua, Italy			
ABI Chromatograms and other information are available on WWW at			
http://grup.bio.unipd.it/ .			
FEATURES			
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1 .93			
/organism="Homo sapiens"			
/db_xref="Taxon:1606"			
/clone="S4000006H09"			
/clone_lib="HM3"			
/sex="female"			
/tissue_type="pectoral muscle (after mastectomy)"			
/note="vector: pCDNA1 (Invitrogen); Site_1: BstXI; Site_2: NotI; The library was constructed by G. Lanfanchi. This library is not subtracted nor normalized: The first strand cDNA was primed with a biotinylated oligo-dT-NotI primer (5'-biotin-AACCGGGTCGAGGGCCGCTTTTTTTTT-3'). The ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected by streptavidin coated magnetic beads, ligated to non-palindromic BstXI adaptors, NotI digested and directionally cloned into BstXI-NotI cut pCDNA1 vector."			
29 a	27 C	26 g	11 t
BASE COUNT			
ORIGIN			
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Best Local Similarity	100.0%	Pred. No. 2.7e+03;	Length 93;
Matches	17;	Mismatches 0;	Pred. No. 2.7e+03;
Conservative		Indels 0;	Gaps 0;
Qy	438	GGCAGGGCTGCCTGG 454	
Db	48	GGGCAGGGCTGCCTGG 32	
DEFINITION			
IMAGE Consortium (info@image.llnl.gov) for further information.			
MGIT:624485			
Seq primer: -28ml3 rev1 ET from Amersham.			
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/strain="C57BL/6"			
/db_xref="taxon:10090"			
/clone IMAGE:1151277			
/clone_lib="Stratagene mouse skin (#937313)"			
/sex="Females"			
/tissue_type="whole skin"			
/dev_stage="11 weeks old"			
/lab_host="SOLR (kanamycin resistant)"			
/note="Organ: skin; Vector: pBluescript SK-; Site_1: EcoRI dt; Site_2: XbaI; Cloned unidirectionally. Primer: Oligo dT. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5', adaptor sequence: 5' GAATTTCGCGCACGG 3' ~3' adaptor sequence: 5' CTCGAGCTTCTTCTTCTT 3' "			
18 a	22 c	30 t	21 g
BASE COUNT			
ORIGIN			
Query Match	1.1%	Score 17;	DB 9;
Best Local Similarity	100.0%	Pred. No. 2.7e+03;	Length 91;
Matches	17;	Mismatches 0;	Indels 0;
Conservative		Gaps 0;	
Qy	919	TGCTGCTCTATGCCGTG 935	
Db	74	TGCTGCTCTATGCCGTG 90	
DEFINITION			
IMAGE Consortium (info@image.llnl.gov) for further information.			
MGIT:624485			
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LOCUS	F24292/C		
DEFINITION	F24292		
VERSION	F24292.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
JOURNAL			
COMMENT			
REFERENCE	1 (bases 1 to 74)		
AUTHORS	Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Kanes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.		
TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
REFERENCE	The Salk Institute for Biological Studies		
AUTHORS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
TITLE			
JOURNAL			
COMMENT			
REFERENCE	1 (bases 1 to 74)		
AUTHORS	Zimmerman,J. and Ecker,J.R.		
TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
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COMMENT	Contact: Joseph R. Ecker		
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COMMENT			
REFERENCE	1 (bases 1 to 74)		
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COMMENT			
REFERENCE	1 (bases 1 to 74)		
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TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
REFERENCE	The Salk Institute for Biological Studies		
AUTHORS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
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JOURNAL			
COMMENT			
REFERENCE	1 (bases 1 to 74)		
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JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
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COMMENT			
REFERENCE	1 (bases 1 to 74)		
AUTHORS	Zimmerman,J. and Ecker,J.R.		
TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
REFERENCE	The Salk Institute for Biological Studies		
AUTHORS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
TITLE			
JOURNAL			
COMMENT			
REFERENCE	1 (bases 1 to 74)		
AUTHORS	Zimmerman,J. and Ecker,J.R.		
TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
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COMMENT			
REFERENCE	1 (bases 1 to 74)		
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JOURNAL			
COMMENT			
REFERENCE	1 (bases 1 to 74)		
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JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
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COMMENT			
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COMMENT	Contact: Joseph R. Ecker		
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COMMENT			
REFERENCE	1 (bases 1 to 74)		
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TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
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AUTHORS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
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JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
REFERENCE	The Salk Institute for Biological Studies		
AUTHORS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
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AUTHORS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
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COMMENT	Contact: Joseph R. Ecker		
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AUTHORS	Zimmerman,J. and Ecker,J.R.		
TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
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COMMENT	Contact: Joseph R. Ecker		
REFERENCE	The Salk Institute for Biological Studies		
AUTHORS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
TITLE			
JOURNAL			
COMMENT			
REFERENCE	1 (bases 1 to 74)		
AUTHORS	Zimmerman,J. and Ecker,J.R.		
TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
REFERENCE	The Salk Institute for Biological Studies		
AUTHORS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
TITLE			
JOURNAL			
COMMENT			
REFERENCE	1 (bases 1 to 74)		
AUTHORS	Zimmerman,J. and Ecker,J.R.		
TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
REFERENCE	The Salk Institute for Biological Studies		
AUTHORS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
TITLE			
JOURNAL			
COMMENT			
REFERENCE	1 (bases 1 to 74)		
AUTHORS	Zimmerman,J. and Ecker,J.R.		
TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
REFERENCE	The Salk Institute for Biological Studies		
AUTHORS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
TITLE			
JOURNAL			
COMMENT			
REFERENCE	1 (bases 1 to 74)		
AUTHORS	Zimmerman,J. and Ecker,J.R.		
TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
REFERENCE	The Salk Institute for Biological Studies		
AUTHORS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
TITLE			
JOURNAL			
COMMENT			
REFERENCE	1 (bases 1 to 74)		
AUTHORS	Zimmerman,J. and Ecker,J.R.		
TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
REFERENCE	The Salk Institute for Biological Studies		
AUTHORS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
TITLE			
JOURNAL			
COMMENT			
REFERENCE	1 (bases 1 to 74)		
AUTHORS	Zimmerman,J. and Ecker,J.R.		
TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
REFERENCE	The Salk Institute for Biological Studies		
AUTHORS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
TITLE			
JOURNAL			
COMMENT			
REFERENCE	1 (bases 1 to 74)		
AUTHORS	Zimmerman,J. and Ecker,J.R.		
TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
REFERENCE	The Salk Institute for Biological Studies		
AUTHORS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
TITLE			
JOURNAL			
COMMENT			
REFERENCE	1 (bases 1 to 74)		
AUTHORS	Zimmerman,J. and Ecker,J.R.		
TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
REFERENCE	The Salk Institute for Biological Studies		
AUTHORS	10010 N. Torrey Pines Road, La Jolla, CA 92037, USA		
TITLE			
JOURNAL			
COMMENT			
REFERENCE	1 (bases 1 to 74)		
AUTHORS	Zimmerman,J. and Ecker,J.R.		
TITLE	A Sequence Indexed Library of Insertion Mutations in the Arabidopsis Genome		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Joseph R. Ecker		
REFERENCE	The Salk Institute for Biological Studies		
AUTHORS	10010 N.		

Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
mtDNA. This sequence lies within an annotated exon of At3g54900.
Class: TDNA tagged.
Location/Qualifiers
1. .74
/organism="Arabidopsis thaliana"
/strain="Columbia Q"
/source="Sanger Center"

Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dhares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gjl4732114 [gb|AF120072.1]), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptorized mouse DNA was annealed to adaptor vector DNA, and transformed into chemically competent *E. coli* XL10-Gold (Stratagene™) cells and selected for ampicillin resistance.

BASE COUNT	22 a	20 c	17 g	15 t	ORIGIN	
Query Match	1.0%	Score 16; DB 17;	Length 74;			
Best Local Similarity	100.0%	Pred. No. 8e+03;				
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Qy	795 CCCAGTTTCAGC 810	AZ783832	76 bp	DNA linear	GSS 16-PFB-2001	
LOCUS	2M0025B16R	Mouse 10kb plasmid UGGCM library	Mus musculus genomic			
DEFINITION	Clone UGGC2M0025B16 R,	DNA sequence.				
ACCESSION	AZ783832	GI:12918803				
VERSION						
KEYWORDS						
SOURCE						
ORGANISM	Mus musculus	Metrazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 76)	Euteleostomi; Murinae; Mus. 1 (bases 1 to 76)			
REFERENCE	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenem,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.	Reid, B., Hamil, C., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenem, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D.				
AUTHORS						
TITLE						
JOURNAL	Unpublished (2000)	Contact: Robert B. Weiss	Insert Length: 10000	SLC, UT		
COMMENT	University of Utah Genome Center	Email: dduinn@genetics.utah.edu	Std Error: 0.00			
	University of Utah	Class: Plasmid ends				
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E.,	High quality sequence stop: 76.				
	84112, USA	Location/Qualifiers				
	Te: 801 585 5606	1. <i>Organism</i> ="Mus musculus"				
	Fax: 801 585 7177	/strain="C57BL/6J"				
FEATURES	source	/note="Organ: leaf; Vector: Rescumeu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; Rescumeu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescumeu, go to the web site: http://www.tcastate.edu and follow the links for "vector" under "vector".				
		/clone_lib="1007 - Rescumeu Grid H"				
		/tissue_type="leaf"				
		/dev_stage="adult"				
		/lab_host="DH10B"				
		/note="Organ: leaf; Vector: Rescumeu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; Rescumeu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescumeu, go to the web site: http://www.tcastate.edu and follow the links for "vector" under "vector".				
		/db_xref="taxon:10090"				
		/clone="UGGC2M0025B16"				
		/sex="Male"				
		/lab_host="E. coli strain XL10-Gold, Ti-resistant, F-				
		/note="Vector: pMD42mv; Purified genomic DNA from M. smegmatis, derived from a recombinant vector containing the rmpA2 gene." data-bbox="978 638 998 904"/>				

'RescueMu', Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT ORIGIN	13 a 23 c	38 g 14 t
Query Match Best Local Similarity 100.0% ; Matches 16; Conservatve 0; Gaps 0;	Score 1.0%; Pred. No. 8.3e+03; Indels 0;	Length 88;
Qy 331 CTGATGAGCTATGG 346 Db 61 CTGATGAGCTATGG 76		

RESULT 9

LOCUS	B39146	91 bp DNA linear GSS 18-OCT-1997
DEFINITION	HS-1049-A1-F09-MR.abi CIR Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 771 Col=17 Row=K, DNA sequence.	
ACCESSION	B39146	
VERSION	1	
KEYWORDS	GI:2543398	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 91)	
REFERENCE	Mahairas, C.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S., Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E.	
AUTHORS		
TITLE	Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Mahairas GC, Zackrone KD, Hood L University of Washington Seattle, WA 98195, USA Tel: (206) 685-8744 Fax: (206) 685-7301 Email: kzackron@u.washington.edu Sequence Tagged Connector Plate: CT 771 row: K column: 17 Class: BAC ends	
FEATURES source	High quality sequence stop: 91. 1..91 Location/Qualifiers	
	/organism="Homo sapiens" (db_xref="Taxon:9606" (clone="Plate=CT 771 Col=17 Row=K" (sex="M" (note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"	
BASE COUNT ORIGIN	21 a 20 c	16 g 34 t

RESULT 10

LOCUS	B1175453	100 bp mRNA linear EST 09-JUL-2001
DEFINITION	OSTR046A5_1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to T20G5_8, mRNA sequence.	
ACCESSION	B1175453	

'RescueMu', Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

BASE COUNT ORIGIN	13 a 23 c	38 g 14 t
Query Match Best Local Similarity 100.0% ; Matches 16; Conservatve 0; Gaps 0;	Score 1.0%; Pred. No. 8.4e+03; Indels 0;	Length 91;
Qy 1380 GAACTCATGATGCCAT 1395 Db 39 GAACTCATGATGCCAT 24		

RESULT 11

LOCUS	AZ492139	36 bp DNA linear GSS 05-OCT-2000
DEFINITION	AZ492139/C Clone UGC1M0326005 F, DNA sequence.	
ACCESSION	AZ492139	
VERSION	AZ492139.1	GI:10664562
KEYWORDS	GSS.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 36)	
REFERENCE	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenah, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederauern, A., and Wright, D., Weiss, R.	
AUTHORS		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	
JOURNAL	Unpublished (2000)	

Db 30 TCTGGTCCTCCCGAG 16

RESULT 14

AU105502/C LOCUS AU105502 Sugano Homo sapiens mRNA linear EST 30-AUG-2001

DEFINITION KAT00658, mRNA sequence.

ACCESSION AU105502

VERSION AU105502.1 GI:13555023

KEYWORDS EST.

SOURCE human

ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE (bases 1 to 50) Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakai Y., Nakamura,Y., Sugano,A. and Sugano,S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072

COMMENT Contact: Yutaka Suzuki

Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
Email: yszukim@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano S., Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES SOURCE

BASE COUNT ORIGIN

Query Match 1.0%; Score 15; DB 9; Length 50;

Best Local Similarity 100.0%; Pred. No. 2.3e+04;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/clone="KAT04851"

/clone-lib="Sugano Homo sapiens cDNA library"

/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"

Query 1280 TCCTGGTCCTCCGAG 1294

11 a 13 c 18 g 8 t

Db 27 TCCTGGTCCTCCGAG 13

Search completed: November 14, 2002, 20:54:33

Job time : 1871 secs

Db 30 TCTGGTCCTCCCGAG 16

RESULT 15

AU105503/C LOCUS AU105503 Sugano Homo sapiens mRNA linear EST 30-AUG-2001

DEFINITION KAT04851, mRNA sequence.

ACCESSION AU105503

VERSION AU105503.1 GI:13555024

KEYWORDS EST.

SOURCE human

ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE (bases 1 to 50) Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakai Y., Nakamura,Y., Sugano,A. and Sugano,S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072

COMMENT Contact: Yutaka Suzuki

Department of Virology

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 14, 2002, 19:30:01 ; search time 61 Seconds
 (without alignments)
 7888.129 Million cell updates/sec

Title: US-09-918-026A-3
 Perfect score: 1569
 Sequence: 1 atggaccaaggggcccg.....cttgcctgcataacctag 1569

Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 1533381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 687286

Minimum DB seq length: 0
 Maximum DB seq length: 100

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	
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2	23	1.5	23	3	US-09-165-042-30	Sequence 30, App	
3	16	1.0	60	3	US-08-911-894-67	Sequence 67, App	
4	16	1.0	89	4	US-08-974-519A-683	Sequence 683, App	
c	5	16	1.0	90	4	US-08-974-519A-684	Sequence 684, App
c	6	15	1.0	17	3	US-08-385-162-144	Sequence 144, App
c	7	15	1.0	20	4	US-09-676-610B-171	Sequence 171, App
c	8	15	1.0	76	2	US-08-482-182-37	Sequence 37, App
c	9	15	1.0	80	2	US-08-482-182-36	Sequence 36, App
c	10	15	1.0	9	1	US-08-111-796-283	Sequence 283, App
c	11	14	0.9	18	3	US-08-471-019-283	Sequence 283, App
c	12	14	0.9	18	3	US-08-487-368A-174	Sequence 445, App
c	13	14	0.9	18	4	US-08-584-040-4455	Sequence 283, App
c	14	14	0.9	18	5	PCT-US3-11198-283	Sequence 54, App
c	15	14	0.9	20	4	US-09-11198-283	Sequence 2, App
c	16	14	0.9	21	4	US-08-940-968-2	Patent No. 5455029
c	17	14	0.9	21	6	5455029-28	Sequence 23, App
c	18	14	0.9	23	4	US-09-182-117-23	Sequence 84, App
c	19	14	0.9	24	3	US-08-890-980-84	Sequence 84, App
c	20	14	0.9	24	3	US-09-032-894-84	Sequence 84, App
c	21	14	0.9	24	4	US-09-031-676-84	Sequence 84, App
c	22	14	0.9	26	4	US-09-255-368-13	Sequence 13, App
c	23	14	0.9	27	1	US-08-111-796-282	Sequence 282, App
c	24	14	0.9	27	1	US-08-758-306-1166	Sequence 1166, App
c	25	14	0.9	27	3	US-08-471-019-282	Sequence 281, App
c	26	14	0.9	27	3	US-08-998-059-231	Sequence 231, App
c	27	14	0.9	27	4	US-09-417-822-19	Sequence 19, App

ALIGNMENTS

RESULT 1
 US-09-165-042-25
 ; Sequence 25, Application US/09165042
 ; Patent No. 6100077
 ; GENERAL INFORMATION:
 ; APPLICANT: Sturley, Stephen L.
 ; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL
 ; TITLE OF INVENTION: ACYLTRANSFERASE
 ; FILE REFERENCE: 0575/56331
 ; CURRENT APPLICATION NUMBER: US/09-165, 042
 ; CURRENT FILING DATE: 1998-10-01
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 25
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: human
 US-09-165-042-25

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Qy 1047 CATGGCTGCTGCATCTCTTGC 10700
 Db 1 CATGGCTGCTGCATCTCTTGC 24

RESULT 2
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 ; Sequence 30, Application US/09165042
 ; Patent No. 6100077
 ; GENERAL INFORMATION:
 ; APPLICANT: Sturley, Stephen L.
 ; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL
 ; TITLE OF INVENTION: ACYLTRANSFERASE
 ; FILE REFERENCE: 0575/56331
 ; CURRENT APPLICATION NUMBER: US/09-165, 042
 ; CURRENT FILING DATE: 1998-10-01
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 30
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: human
 US-09-165-042-30

Query Match Best Local Similarity 100.0%; Pred. No. 0.052; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1539 GACCTCTGATCTGGTCCTGCC 1561
 Db 1 GACCTCTGATCTGGTCCTGCC 23

RESULT 3

US-08-911-894-67

Sequence 67, Application US/08911894

Patent No. 6030840

GENERAL INFORMATION:

APPLICANT: Saxon, Andrew

APPLICANT: Zhang, Ke

APPLICANT: Fujieda, Shigebaru

TITLE OF INVENTION: IMMUNOGLOBULIN TRANS-SPliced TRANSCRIPTS

TITLE OF INVENTION: IMMUNOGLOBULIN TRANS-SPliced TRANSCRIPTS

NUMBER OF SEQUENCES: 90

CORRESPONDENCE ADDRESS:

ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld

STREET: 816 Congress Avenue, Suite 1900

CITY: Austin

STATE: Texas

ZIP: 78701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.10

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/911-894

FILING DATE: CONCURRENTLY Herewith

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/023,579

FILING DATE: 19-AUG-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Mayfield, Denise L.

REGISTRATION NUMBER: 33,732

REFERENCE/DOCKET NUMBER: 43496.0006

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 499-6200

TELEFAX: (512) 499-6290

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 60 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLogy: linear

US-08-911-894-67

Query Match 1.0%; Score 16; DB 3; Length 60;

Best Local Similarity 100.0%; Pred. No. 3.3e-02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 GCAGAGCACAGAGGG 45
 Db 40 GCAGAGCACAGAGGG 55

RESULT 4

US-08-974-549A-683

Sequence 683, Application US/08974549A

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.

NAME/KEY: ;
 LOCATION: 1..89
 OFFER INFORMATION: /note= "oligonucleotide 21B"
 US-08-974-549A-683

Query Match 1.0%; Score 16; DB 4; Length 89;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;

Qy 471 CTTCAAGCTTCGGACAG 486
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 Db 57 CTTCAGCTTCGGACAG 72

RESULT 5
 ; Sequence 684, Application US/08974549A
 ; Patent No. 616617B
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 APPLICANT: Lingner, Joachim
 APPLICANT: Nakamura, Toru
 APPLICANT: Chapman, Karen B.
 APPLICANT: Morin, Gregg B.
 APPLICANT: Harley, Calvin B.
 APPLICANT: Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 727
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/974,549A
 FILING DATE: 19-NOV-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724, 643
 FILING DATE: 01-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/911,312
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/915,503
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/17618
 FILING DATE: 01-OCT-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph Ted
 REGISTRATION NUMBER: 36,429
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 684:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..90
; OTHER INFORMATION: /note= "Oligonucleotide 21T"
; US-08-974-549A-684

Query Match 1.0%; Score 16; DB 4; Length 90;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 471 CTTCAAGCTTCGGACAG 486
 Qy 471 CTTCAAGCTTCGGACAG 486
 Db 43 CTTCAAGCTTCGGACAG 28

RESULT 6
 US-08-985-162-144/C
 ; Sequence 144, Application US/08985162
 ; GENERAL INFORMATION:
 / APPLICANT: Akhtar, Saghir
 / APPLICANT: Fell, Patricia
 / APPLICANT: McSwiggen, James
 / TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
 / TITLE OF INVENTION: OF DISEASES OR CONDITION RELATED
 / TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
 / TITLE OF INVENTION: FACTOR RECEPTORS
 / NUMBER OF SEQUENCES: 1877
 / CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 623 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: EASTSEQ for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/985,162
 FILING DATE: 04-December-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/036,476
 FILING DATE: 31-January-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 230/107
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 499-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 144:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 17 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-985-162-144

Query Match 1.0%; Score 15; DB 3; Length 17;

Best Local Similarity 100.0%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0;

Qy 340 CCGATGGGTCGAG 354
 Db 15 CGATGGGGTCGAG 1

RESULT 7
 US-09-487-368A-174/c
 Sequence 174, Application US/09487368A
 ; GENERAL INFORMATION:
 ; APPLICANT: Lex M. Cowser
 ; TITLE OF INVENTION: RTS-0093 ANTISENSE MODULATION OF PTP1B EXPRESSION
 ; CURRENT APPLICATION NUMBER: US/09/487-368A
 ; CURRENT FILING DATE: 2000-01-18
 ; NUMBER OF SEQ ID NOS: 240
 ; SEQ ID NO: 174
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-487-368A-174

Query Match 1.0%; Score 15; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0;

Qy 245 TGGCCCCACCTCCCC 259
 Db 20 TGCCCCCACCTCCCC 6

RESULT 8
 US-09-676-610B-171
 Sequence 171, Application US/09676610B
 ; GENERAL INFORMATION:
 ; APPLICANT: C. Frank Bennett
 ; APPLICANT: Jacqueline Wyatt
 ; APPLICANT: Susan M. Freier
 ; TITLE OF INVENTION: OLIGONUCLEOTIDE INHIBITION OF HER-1 EXPRESSION
 ; FILE REFERENCE: RTS-0138
 ; CURRENT APPLICATION NUMBER: US/09/676,610B
 ; CURRENT FILING DATE: 2000-09-29
 ; NUMBER OF SEQ ID NOS: 182
 ; SEQ ID NO: 171
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-676-610B-171

Query Match 1.0%; Score 15; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0;

APPLICANT: OLSON, PAMELA S.
 TITLE OF INVENTION: CHROMOSOMAL EXPRESSION OF HETEROLOGOUS GENES IN BACTERIAL CELLS
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,182
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PARK, FREDDIE K.
 REGISTRATION NUMBER: 35,636
 REFERENCE/DOCKET NUMBER: 22095-20281.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0790
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 76 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-482-182-37

Query Match 1.0%; Score 15; DB 2; Length 76;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1059 CATCTCTTGCGTT 1073
 Db 45 CATCTCTTGCGTT 59

RESULT 10
 US-08-482-182-36/c
 Sequence 36, Application US/08482182
 ; Patent No. 5861273
 ; GENERAL INFORMATION:
 ; APPLICANT: MASCARENHAS, DESMOND
 ; APPLICANT: OLSON, PAMELA S.
 ; TITLE OF INVENTION: CHROMOSOMAL EXPRESSION OF HETEROLOGOUS GENES IN BACTERIAL CELLS
 ; NUMBER OF SEQUENCES: 81
 ; CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,182
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PARK, FREDDIE K.

RESULT 9
 US-08-482-182-37
 Sequence 37, Application US/08482182
 ; Patent No. 5861273
 ; GENERAL INFORMATION:
 ; APPLICANT: MASCARENHAS, DESMOND

REGISTRATION NUMBER: 35,636
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 80 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-482-182-36

Query Match Score 1.08; Best Local Similarity 100.0%; Pred. No. 9.7e-02; Length 80; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0; RESULT 12
 US-08-471-039-283

Qy 1059 CATCTCTTGGCCTT 1073
 Db 40 CATCTCTTGGCCTT 26

RESULT 11
 US-08-411-796-283

; Sequence 283, Application US/08411796
 ; Patent No. 5677149

GENERAL INFORMATION:
 APPLICANT: Abrams, Mark A.
 APPLICANT: Bauer, S.C.
 APPLICANT: Bradford-Goldberg, Sarah R.
 APPLICANT: Caparon, Maire H.
 APPLICANT: Easton, Alan M.
 APPLICANT: Klein, Barbara K.
 APPLICANT: McKearn, John P.
 APPLICANT: Oliins, Peter O.
 APPLICANT: Paik, Kumanan
 APPLICANT: Polazzi, Joseph O.
 APPLICANT: Thomas, John W.

TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides
 NUMBER OF SEQUENCES: 549
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
 STREET: P. O. Box 5110
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60680

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/411,796
 FILING DATE: 22-NOV-1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/981044
 FILING DATE: 24-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/11198
 FILING DATE: 22-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Bennett, Dennis A.
 REGISTRATION NUMBER: 34,547
 REFERENCE/DOCKET NUMBER: C2713/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (708)470-6501
 FAX: (708)470-6881
 INFORMATION FOR SEQ ID NO: 283:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (synthetic)
 US-08-471-039-283

REGISTRATION NUMBER: 35,636
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 80 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-411-796-283

Query Match Score 0.9%; Best Local Similarity 100.0%; Pred. No. 3e+03; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0; RESULT 12
 US-08-471-039-283

Qy 1548 ATCTTGCTCTGCC 1561
 Db 1 ATCTTGCTCTGCC 14

GENERAL INFORMATION:
 APPLICANT: Abrams, Mark A.
 APPLICANT: Bauer, S.C.
 APPLICANT: Bradford-Goldberg, Sarah R.
 APPLICANT: Caparon, Maire H.
 APPLICANT: Easton, Alan M.
 APPLICANT: Klein, Barbara K.
 APPLICANT: McKearn, John P.
 APPLICANT: Oliins, Peter O.
 APPLICANT: Paik, Kumanan
 APPLICANT: Polazzi, Joseph O.
 APPLICANT: Thomas, John W.

TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides
 NUMBER OF SEQUENCES: 549
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
 STREET: P. O. Box 5110
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60680

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,039
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/981,044
 FILING DATE: 24-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/11198
 FILING DATE: 22-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Bennett, Dennis A.
 REGISTRATION NUMBER: 34,547
 REFERENCE/DOCKET NUMBER: C2713/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (708)470-6501
 FAX: (708)470-6881
 INFORMATION FOR SEQ ID NO: 283:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (synthetic)
 US-08-471-039-283

Query Match 0.9%; Score 14; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3e+03; 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1548 ATCTTGGTCCTGCC 1561
 Db 1 ATCTTGGTCCTGCC 14

RESULT 13
 US-08-584-040-4455
 Sequence 4455, Application US/08584040
 Patent No. 6346398

GENERAL INFORMATION:
 APPLICANT: McSwiggen, James S.
 APPLICANT: Stinchcomb, Dan T.
 APPLICANT: Escobedo, Jaime
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF VASCULAR ENDOTHELIAL GROWTH FACTOR

TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL GROWTH FACTOR

NUMBER OF SEQUENCES: 8502

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 COMPUTER: IBM compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/584,040
 FILING DATE: January 11, 1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/005,974
 FILING DATE: October 26, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 4455:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 STRANDEDNESS: linear

US-08-584-040-4455

Query Match 0.9%; Score 14; DB 4; Length 18;
 Best Local Similarity 78.6%; Pred. No. 3e+03; 0; Gaps 0;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 945 GGCGCCGCTTG 958
 Db 3 GGCGCCGCTTG 16

RESULT 14
 PC/US93-11198-283
 Sequence 283, Application PC/TUS9311198

GENERAL INFORMATION:
 APPLICANT: Abrams, Mark A.
 APPLICANT: Bauer, S. C.
 APPLICANT: Bradford-Goldberg, Sarah R.
 APPLICANT: Caparon, Maire H.
 APPLICANT: Easton, Alan M.
 APPLICANT: Klein, Barbara K.
 APPLICANT: McKearn, John P.
 APPLICANT: Ollins, Peter O.
 APPLICANT: Paik, Kunman
 APPLICANT: Polazzi, Joseph O.
 APPLICANT: Thomas, John W.
 TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides

NUMBER OF SEQUENCES: 549

CORRESPONDENCE ADDRESS:
 APPLICANT: Dennis A. Bennett, G.D. Searle & Co., ADDRESSEE: Corporate Patent Dept.
 STREET: P.O. Box 5110
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60680

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/11198
 FILING DATE: 1993-07-01
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/981044
 FILING DATE: 24-NOV-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Bennett, Dennis A.
 REGISTRATION NUMBER: 34,547
 REFERENCE/DOCKET NUMBER: C2713/1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (708)470-6501
 TELEFAX: (708)470-6881
 INFORMATION FOR SEQ ID NO: 283:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (synthetic)

PCT/US93-11198-283

Query Match 0.9%; Score 14; DB 5; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3e+03; 0; Gaps 0;

Qy 1548 ATCTTGGTCCTGCC 1561
 Db 1 ATCTTGGTCCTGCC 14

RESULT 15
 US-09-851-520-54/C
 Sequence 54, Application US/09851520
 Patent No. 6399379
 GENERAL INFORMATION:
 APPLICANT: Brenda F. Baker
 APPLICANT: Susan M. Freier
 TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
 FILE REFERENCE: RTI-0241
 CURRENT APPLICATION NUMBER: US/09/851,520
 CURRENT FILING DATE: 2001-05-07
 NUMBER OF SEQ ID NOS: 88
 SEQ ID NO 54
 LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: Antisense Oligonucleotide
; OTHER INFORMATION: Antisense Oligonucleotide
us-09-851-320-54

Query Match 0.9%; Score 14; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 332 TTGATGAGCTGATG 345
 |||||||
Db 15 TTGATGAGCTGATG 2

Search completed: November 14, 2002, 20:55:54
Job time : 63 secs

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